



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Coughlin, Shaun
Ishihari, Hiroaki
Connolly, Andrew
- (ii) TITLE OF THE INVENTION: Protease Activated Receptor
3 and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/208,629
(B) FILING DATE: 08-DEC-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/742,440
(B) FILING DATE: 30-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Catherine M. Polizzi
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(C) REFERENCE/DOCKET NUMBER: 220002060310
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTTTGTA	TACTTAACRA	CATCCTGTAG	CCGGGTCTCA	GGACATCAAG	ATGAAAATCC	60
TTATCTTGGT	TGCAGCTGGG	CTGCTGTTTC	TGCCAGTCAC	TGTTTGCCAA	AGTGGCATAA	120
ATGTTTCAGA	CAACTCAGCA	AAGCCAACCT	TAACTATTAA	GAGTTTAAAT	GGGGGTCCCC	180
AAAATACCTT	TGAAGAATTC	CCACTTTCTG	ACATAGAGGG	CTGGACAGGA	GCCACCACAA	240
CTATAAAAGC	GGAGTGTCCC	GAGGACAGTA	TTTCAACTCT	CCACGTGAAT	AATGCTACCA	300
TAGGATACCT	GAGAAGTTCC	TTAAGTACCC	AAGTGATACC	TGCCATCTAT	ATCCTGCTGT	360
TTGTGGTTGG	TGTACCATCC	AACATCGTGA	CCCTGTGGAA	ACTCTCCTTA	AGGACCAAAT	420
CCATCAGTCT	GGTCATCTTT	CACACCAACC	TGGCCATCGC	AGATCTCCTT	TTCTGTGTCA	480
CACTGCCATT	TAAGATCGCC	TACCATCTCA	ATGGCAACAA	CTGGGTATTT	GGCGAGGTCA	540
TGTGCCGGAT	CACCACGGTC	GTTTCTACG	GCAACATGTA	CTGCGCTATC	CTGATCCTCA	600
CTTGCAAGGG	CATCAACCGC	TACCTGGCCA	CGGCTCACCC	TTTCACATA	CAGAAGCTGC	660
CCAAACGCAG	CTTCTCCTTG	CTCATGTGTG	GCATAGTGTG	GGTCATGGTT	TTCTTATACA	720
TGCTGCCCTT	TGTCATCCTG	AAGCAGGAGT	ACCACCTCGT	CCACTCAGAG	ATCACCACCT	780
GCCACGATGT	CGTCGACGCG	TGCGAGTCCC	CATCATCCTT	CCGATTCTAC	TACTTCGTCT	840
CCTTAGCATT	CTTTGGGTTT	CTCATCCCGT	TTGTGATCAT	CATCTTCTGT	TACACGACTC	900
TCATCCACAA	ACTTAAATCA	AAGGATCGGA	TATGGCTGGG	CTACATCAAG	GCCGTCCTCC	960
TCATCCTTGT	GATTTTCACA	ATTTGCTTTG	CCCCACCAA	CATCATACTC	GTAATCCACC	1020
ATGCCAACTA	CTACTACCAC	AATACCGACA	GCTTGTAATT	TATGTATCTT	ATTGCTCTGT	1080
GCCTGGGGAG	CCTGAATAGC	TGCCTAGATC	CATTCCCTTA	CTTTGTCATG	TCGAAAGTTG	1140
TAGATCAGCT	TAATCCTTAG	TCGGCAATGG	CAAGACCACT	TTAGAGACCA	AGGAGAGATA	1200
TCTGGGAAGA	CATACATGCT	TGGC				1224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1124
- (D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATATGCTA	ATATTTCTTT	TCAATTACAG	GCATAAATGT	TTCAGACAAC	TCAGCAAAGC	60
CAACCTTAAC	TATTAAGAGT	TTTAATGGGG	GTCCCCAAAA	TACCTTTGAA	GAATTCNNNN	120
NNNTACAAC	CTCCATGTGA	ATAATGCTAC	CATGGGATAC	CTGAGAGTT	CCTTAAGTAC	180
CAAAGTGATA	CCTGCCATCT	ACATCCTGGT	GTTTGTGATT	GGTGTAACAG	CGAACATCGT	240
GACCCTGTGG	AAACTCTCCT	CAAGGACCAA	ATCCATCTGT	CTGGTCATCT	TTACACCCAA	300
CCTGGCCATC	GCGGATCTCC	TTTTCTGTGT	CACGCTGCCG	TTTAAGATCN	NCCTACCATC	360
TCAATGGCAA	CAACTGGGTA	TTTGGCGAGG	TCATGTGCCG	GATCACCACC	GTCGTTTTCT	420
ACGGCAACAT	GTAATGCGCT	ANNNTCCTGA	TCCTCACCTG	CATGGGCATC	AACCGCTACC	480
TGGCCACGGC	TCACCCTTTC	ACATACCAGA	AGCTGCCCAA	ACGCAGCTTC	TCCATGCTCA	540
TGTGTGGCAT	GGTGTGGGTC	ATGGTTTTCT	TATACATGCT	GCCCTTTGTC	ATCCNNNAAG	600

CAGGAGTACC	ACCTCGTCCA	CTCCGAGATC	ACCACCTGCC	ACGATGTCGT	CGACGCGTGC	660
GANTCCCCAT	CATCCTTCCG	ATTCTACTAC	TTCGTCTCCT	TAGCATTCTT	TGGGTTCTCT	720
ATCCCGTTTG	TGATCATCAT	CTTCTGTTAC	ACGACTCTCA	TCCACAAACT	TAAATCAAAA	780
GATCNGATAT	GGCTGGGCTA	CATCAAGGCC	GTCCTCCTCA	TCCTTGTGAA	TTTCACCATC	840
TGCTTCCCCC	CCAQCAAGNN	NNMNGATATC	TGGGAAGACG	TACATGCTTG	GCTGACTTGT	900
GCATGGCACC	ATCAGCTCAA	TTTTTAATTT	TTTAATTTTA	ATTTAATTTA	ATTTTATGTT	960
TTTGAGACAG	AGCCTCACTG	TGTAGTCCTG	GCTGGCCTGG	CTGGTTCTCT	ATTTAGACCA	1020
GGTTAGCCTT	GAAGTCACAG	AGATCTGCCT	GCTTCTGCCT	CCCAAGTGCT	GGGTTCAACC	1080
AGGTCTGGCA	AGCGCTCCAT	TTTTTCAGCTC	CTCTGCAACA	GTGC		1124

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Leu Tyr Thr

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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TGCTCCATGA	TTTTACAGAT	TTCATAACGT	TTAAGAGACG	GGACTCAGGT	CATCAAAATG	60
AAAGCCCTCA	TCTTTGCAGC	TGCTGGCCTC	CTGCTTCTGT	TGCCCCTTTT	TTGTCAGAGT	120
GGCATGGAAA	ATGATACAAA	CAACTTGGCA	AAGCCAACCT	TACCCATTAA	GACCTTTCGT	180
GGAGCTCCCC	CAAATTCTTT	TGAAGAGTTC	CCCTTTTCTG	CCTTGGAAGG	CTGGACAGGA	240
GCCACGATTA	CTGTAAAAAT	TAAGTGCCCT	GAAGAAAGTG	CTTCACATCT	CCATGTGAAA	300
AATGCTACCA	TGGGGTACCT	GACCAGCTCC	TTAAGTACTA	AACTGATACC	TGCCATCTAC	360
CTCCTGGTGT	TTGTAGTTGG	TGTCCCGGCC	AATGCTGTGA	CCCTGTGGAT	GCTTTTCTTC	420
AGGACCAGAT	CCATCTGTAC	CACTGTATTC	TACACCAACC	TGGCCATTGC	AGATTTTCTT	480
TTTTGTGTTA	CATTGCCCTT	TAAGATAGCT	TATCATCTCA	ATGGGAACAA	CTGGGTATTT	540
GGAGAGGTCC	TGTGCCGGGC	CACCACAGTC	ATCTTCTATG	GCAACATGTA	CTGCTCCATT	600
CTGCTCCTTG	CCTGCATCAG	CATCAACCGC	TACCTGGCCA	TCGTCCATCC	TTTCACCTAC	660
CGGGGCCTGC	CCAAGCACAC	CTATGCCTTG	GTAACATGTG	GACTGGTGTG	GGCAACAGTT	720
TTCTTATATA	TGCTGCCATT	TTTCATACTG	AAGCAGGAAT	ATTATCTTGT	TCAGCCAGAC	780
ATCACCACCT	GCCATGATGT	TCACAACACT	TGCGAGTCCT	CATCTCCCTT	CCAACCTAT	840
TACTTCATCT	CCTTGGCATT	CTTTGGATTG	TTAATTCCAT	TTGTGCTTAT	CATCTACTGC	900
TATGCAGCCA	TCATCCGGAC	ACTTAATGCA	TACGATCATA	GATGGTTGTG	GTATGTTAAG	960
GCGAGTCTCC	TCATCCTTGT	GATTTTACC	ATTGTCTTTG	CTCCAAGCAA	TATTATTCCT	1020
ATTATTCACC	ATGCTAAGTA	CTACTACAAC	AACACTGATG	GCTTATATTT	TATATATCTC	1080
ATAGCTTTGT	GCCTGGGTAG	TCTTAATAGT	TGCTTAGATC	CATTCTTTTA	TTTTCTCATG	1140
TCAAAAACCA	GAAATCACTC	CACTGCTTAC	CTTACAAAAT	AGTGAAATGA	TCTTAGAGAA	1200
CAAGGACAGC	CATCACAGAG	AACG				1224

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGGCATGG AAAATGATAC AAACAACCTTG GCAAAGCCAA CCTTACCCAT TAAGACCTTT 60
CGTGGAGCTC CCCCAATTTC TTTTGAAGAG TTCCCCTTTT CTGCCTTGGA AGGCTGGACA 120
GGAGCCACGA TTAAGTAAA AATTAAGTGC CCTGAAGAAA GTGCTTCACA TCTCCATGTG 180
AAAAATGCTA CCATGGGGTA CCTGACCAGC TCCTTAAGTA CTAAACTGAT ACCTGCCATC 240
TACCTCCTGG TGTGTGTAGT TGGTGTCCCG GCCAATGCTG TGACCCTGTG GATGCTTTTC 300
TTCAGGACCA GATCCATCTG TACCACTGTA TTCTACACCA ACCTGGCCAT TGCAGATTTT 360
CTTTTTTGTG TTACATTGCC CTTTAAGATA GCTTATCATC TCAATGGGAA CAACTGGGTA 420
TTTGGAGAGG TCCTGTGCCG GGCCACCACA GTCATCTTCT ATGGCAACAT GTACTGCTCC 480
ATTCTGCTCC TTGCCTGCAT CAGCATCAAC CGCTACCTGG CCATCGTCCA TCCTTTCACC 540
TACCGGGGCC TGCCCAAGCA CACCTATGCC TTGGTAACAT GTGGACTGGT GTGGGCAACA 600
GTTTTCTTAT ATATGCTGCC ATTTTTCATA CTGAAGCAGG AATATTATCT TGTTCAAGCA 660
GACATACCA CCTGCCATGA TGTTCACAAC ACTTGCAGT CCTCATCTCC CTTCCAACTC 720
TATTACTTCA TCTCCTTGGC ATTCTTTGGA TTCTTAATTC CATTTGTGCT TATCATCTAC 780
TGCTATGCAG CCATCATCCG GACACTTAAT GCATACGATC ATAGATGGTT GTGGTATGTT 840
AAGGCGAGTC TCCTCATCCT TGTGATTTT ACCATTTGCT TTGCTCCAAG CAATATTATT 900
CTTATTATTC ACCATGCTAA CTACTACTAC AACAACACTG ATGGCTTATA TTTTATATAT 960
CTCATAGCTT TGTGCCTGGG TAGTCTTAAT AGTTGCTTAG ATCCATTCTT TTTTCTCTC 1020
ATGTCAAAAA CCAGAAATCA CTCCACTGCT TACCTTACAA AATAGTGAAA TGATCTTAGA 1080
GAACAAGGAC AGCCATCACA GA 1102

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Ser Met Ile Leu Gln Ile Ser

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys
1 5 10 15

Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys
 20 25 30
 Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
 35 40 45
 Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
 50 55 60
 Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu
 65 70 75 80
 Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu
 85 90 95
 Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val
 100 105 110
 Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile
 115 120 125
 Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu
 130 135 140
 Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser
 145 150 155 160
 Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg
 165 170 175
 Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu Leu
 180 185 190
 Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met
 195 200 205
 Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu
 210 215 220
 Ala Ile Trp Ala Leu Ala Ile Ala Gly Val Val Pro Leu Val Leu Lys
 225 230 235 240
 Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr Cys His Asp
 245 250 255
 Val Leu Asn Glu Thr Leu Leu Glu Gly Tyr Tyr Ala Tyr Tyr Phe Ser
 260 265 270
 Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu Ile Ile Ser Thr Val
 275 280 285
 Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ser Ala Val Ala Asn
 290 295 300
 Arg Ser Lys Lys Ser Arg Ala Leu Phe Leu Ser Ala Ala Val Phe Cys
 305 310 315 320
 Ile Phe Ile Ile Cys Phe Gly Pro Thr Asn Val Leu Leu Ile Ala His
 325 330 335
 Tyr Ser Phe Leu Ser His Thr Ser Thr Thr Glu Ala Ala Tyr Phe Ala
 340 345 350
 Tyr Leu Leu Cys Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro
 355 360 365
 Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser
 370 375 380
 Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser
 385 390 395 400
 Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn
 405 410 415
 Asn Ser Ile Tyr Lys Lys Leu Leu Thr
 420 425

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Ser Pro Ser Ala Ala Trp Leu Leu Gly Ala Ala Ile Leu Leu
 1 5 10 15
 Ala Ala Ser Leu Ser Cys Ser Gly Thr Ile Gln Gly Thr Asn Arg Ser
 20 25 30
 Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val
 35 40 45
 Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe
 50 55 60
 Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Ile
 65 70 75 80
 Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met Ala
 85 90 95
 Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile
 100 105 110
 Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe
 115 120 125
 Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly
 130 135 140
 Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr
 145 150 155 160
 Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val
 165 170 175
 Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile
 180 185 190
 Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile Pro
 195 200 205
 Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr
 210 215 220
 Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Pro Phe
 225 230 235 240
 Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe Leu Thr Ala
 245 250 255
 Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser Ala Met Asp
 260 265 270
 Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu Ile Val Thr
 275 280 285
 Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn Leu Leu Leu
 290 295 300
 Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser His Val Tyr
 305 310 315 320
 Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile
 325 330 335
 Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala
 340 345 350
 Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln
 355 360 365
 Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Ser Tyr Ser
 370 375 380

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Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
385 390

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...29
- (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24

- (A) NAME/KEY: Other
- (B) LOCATION: 22...27
- (D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTNTACATGC TNMACYTNGC NNTNGCNGA

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 6...21
- (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, and 21

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 24
- (D) OTHER INFORMATION: N=A or C or G or T at residue 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGATANACNA CNGCNADRWA NCKNTC

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Tyr Lys Asp Asp Asp
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
1 5 10 15
Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr
20 25 30
Lys Asp Asp Asp Asp Val Glu
35

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Glu Glu Phe Pro
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Thr Pro Lys

1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Phe Arg Gly Ala Pro

1

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
 1 5 10 15
 Phe Pro Phe Ser Ala Leu Glu
 20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Pro Ile Lys Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
 1 5 10 15
 Phe Pro Phe Ser Ala Leu Glu
 20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Pro Ile Xaa Thr Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu
 1 5 10 15
 Glu Phe Pro Phe Ser Ala Leu Glu
 20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Xaa Pro Arg Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe
 1 5 10 15
 Pro Phe Ser Ala Leu Glu
 20

(2) INFORMATION FOR SEQ ID NO:22:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Pro Ile Lys

1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gln His Pro Val Ala Gly Ser Gln Asp Ile Lys Met Lys Ile Leu Ile
1 5 10 15
Leu Val Ala Ala Gly Leu Leu Phe Leu Pro Val Thr Val Cys Gln Ser
20 25 30
Gly Ile Asn Val Ser Asp Asn Ser Ala Lys Pro Thr Leu Thr Ile Lys
35 40 45
Ser Phe Asn Gly Gly Pro Gln Asn Thr Phe Glu Glu Phe Pro Leu Ser
50 55 60
Asp Ile Glu Gly Trp Thr Gly Ala Thr Thr Thr Ile Lys Ala Glu Cys
65 70 75 80
Pro Glu Asp Ser Ile Ser Thr Leu His Val Asn Asn Ala Thr Ile Gly
85 90 95
Tyr Leu Arg Ser Ser Leu Ser Thr Gln Val Ile Pro Ala Ile Tyr Ile
100 105 110
Leu Leu Phe Val Val Gly Val Pro Ser Asn Ile Val Thr Leu Trp Lys
115 120 125
Leu Ser Leu Arg Thr Lys Ser Ile Ser Leu Val Ile Phe His Thr Asn
130 135 140

Leu Ala Ile Ala Asp Leu Leu Phe Cys Val Thr Leu Pro Phe Lys Ile
 145 150 155 160
 Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe Gly Glu Val Met Cys
 165 170 175
 Arg Ile Thr Thr Val Val Phe Tyr Gly Asn Met Tyr Cys Ala Ile Leu
 180 185 190
 Ile Leu Thr Cys Met Gly Ile Asn Arg Tyr Leu Ala Thr Ala His Pro
 195 200 205
 Phe Thr Tyr Gln Lys Leu Pro Lys Arg Ser Phe Ser Leu Leu Met Cys
 210 215 220
 Gly Ile Val Trp Val Met Val Phe Leu Tyr Met Leu Pro Phe Val Ile
 225 230 235 240
 Leu Lys Gln Glu Tyr His Leu Val His Ser Glu Ile Thr Thr Cys His
 245 250 255
 Asp Val Val Asp Ala Cys Glu Ser Pro Ser Ser Phe Arg Phe Tyr Tyr
 260 265 270
 Phe Val Ser Leu Ala Phe Phe Gly Phe Leu Ile Pro Phe Val Ile Ile
 275 280 285
 Ile Phe Cys Tyr Thr Thr Leu Ile His Lys Leu Lys Ser Lys Asp Arg
 290 295 300
 Ile Trp Leu Gly Tyr Ile Lys Ala Val Leu Leu Ile Leu Val Ile Phe
 305 310 315 320
 Thr Ile Cys Phe Ala Pro Thr Asn Ile Ile Leu Val Ile His His Ala
 325 330 335
 Asn Tyr Tyr Tyr His Asn Thr Asp Ser Leu Tyr Phe Met Tyr Leu Ile
 340 345 350
 Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu Asp Pro Phe Leu Tyr
 355 360 365
 Phe Val Met Ser Lys Val Val Asp Gln Leu Asn Pro
 370 375 380

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Ala Met Ala Arg Pro Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Pro Arg Arg Asp Ile Trp Glu Asp Ile His Ala Trp
 1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg Leu Arg Asp Gly Thr Gln Val Ile Lys Met Lys Ala Leu Ile Phe
1 5 10 15
Ala Ala Ala Gly Leu Leu Leu Leu Pro Thr Phe Cys Gln Ser Gly
20 25 30
Met Glu Asn Asp Thr Asn Asn Leu Ala Lys Pro Thr Leu Pro Ile Lys
35 40 45
Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe Pro Phe Ser
50 55 60
Ala Leu Glu Gly Trp Thr Gly Ala Thr Ile Thr Val Lys Ile Lys Cys
65 70 75 80
Pro Glu Glu Ser Ala Ser His Leu His Val Lys Asn Ala Thr Met Gly
85 90 95
Tyr Leu Thr Ser Ser Leu Ser Thr Lys Leu Ile Pro Ala Ile Tyr Leu
100 105 110
Leu Val Phe Val Val Gly Val Pro Ala Asn Ala Val Thr Leu Trp Met
115 120 125
Leu Phe Phe Arg Thr Arg Ser Ile Cys Thr Thr Val Phe Tyr Thr Asn
130 135 140
Leu Ala Ile Ala Asp Phe Leu Phe Cys Val Thr Leu Pro Phe Lys Ile
145 150 155 160
Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe Gly Glu Val Leu Cys
165 170 175
Arg Ala Thr Thr Val Ile Phe Tyr Gly Asn Met Tyr Cys Ser Ile Leu
180 185 190
Leu Leu Ala Cys Ile Ser Ile Asn Arg Tyr Leu Ala Ile Val His Pro
195 200 205
Phe Thr Tyr Arg Gly Leu Pro Lys His Thr Tyr Ala Leu Val Thr Cys
210 215 220
Gly Leu Val Trp Ala Thr Val Phe Leu Tyr Met Leu Pro Phe Phe Ile
225 230 235 240
Leu Lys Gln Glu Tyr Tyr Leu Val Gln Pro Asp Ile Thr Thr Cys His
245 250 255
Asp Val His Asn Thr Cys Glu Ser Ser Ser Pro Phe Gln Leu Tyr Tyr
260 265 270
Phe Ile Ser Leu Ala Phe Phe Gly Phe Leu Ile Pro Phe Val Leu Ile
275 280 285
Ile Tyr Cys Tyr Ala Ala Ile Ile Arg Thr Leu Asn Ala Tyr Asp His
290 295 300
Arg Trp Leu Trp Tyr Val Lys Ala Ser Leu Leu Ile Leu Val Ile Phe
305 310 315 320
Thr Ile Cys Phe Ala Pro Ser Asn Ile Ile Leu Ile Ile His His Ala
325 330 335
Asn Tyr Tyr Tyr Asn Asn Thr Asp Gly Leu Tyr Phe Ile Tyr Leu Ile
340 345 350
Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu Asp Pro Phe Leu Tyr
355 360 365

Sub
EI
cont

Phe Leu Met Ser Lys Thr Arg Asn His Ser Thr Ala Tyr Leu Thr Lys
 370 375 380

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asn Asp Leu Arg Glu Gln Gly Gln Pro Ser Gln Arg Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Gly Ser Gly Met Glu Asn Asp Thr Asn Asn Leu Ala Lys Pro Thr
 5 10 15
 Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
 20 25 30
 Phe Pro Phe Ser Ala Leu Glu Gly Trp Thr Gly Ala Thr Ile Thr Val
 35 40 45
 Lys Ile Lys Cys Pro Glu Glu Ser Ala Ser His Leu His Val Lys Asn
 50 55 60
 Ala Thr Met Gly Tyr Leu Thr Ser Ser Leu Ser Thr Val Glu His His
 65 70 75 80
 His His His His

*Sub
E1
cont*

D2